Amendments to the Specification

Please replace the title of the invention with the following amended title:

DNA MOLECULES ENCODING BETA CLAMP ~~DNA REPLICATION~~ PROTEINS OF GRAM POSITIVE BACTERIA ~~AND THEIR USE TO SCREEN FOR CHEMICAL INHIBITORS~~

Please replace the paragraph at page 1, lines 4–108 with the following amended paragraph:

The present application is a national stage application under 35 U.S.C. 371 of PCT US00/020666, which is a continuation-in-part of U.S. Patent Application Serial No. 09/235,245 filed January 22, 1999, now abandoned, which claims benefit of U.S. Provisional Patent Application Serial No. 60/093,727 filed July 22, 1998, and U.S. Provisional Patent Application Serial No. 60/074,522 filed January 22, 1998, all of which are hereby incorporated by reference. The present application also claims benefit of U.S. Provisional Patent Application Serial No. 60/146,178 filed July 29, 1999, which is hereby incorporated by reference.

Please replace the paragraph at page 21, lines 25–28 with the following amended paragraph:

Figure 9 compares the homology between the polypeptide encoded by *dnaE* of *S. aureus* and other organisms. An alignment is shown for the amino acid sequence of the *S. aureus dnaE* product (SEQ. ID. No. 85) with the *dnaE* products (alpha subunits) of *E. coli* (SEQ. ID. No. 86) and *Salmonella typhimurium* (SEQ. ID. No. 87).

Please replace the paragraph at page 21, lines 29–32 with the following amended paragraph:

Figure 10 compares the homology between the N-terminal regions of the gamma/tau polypeptides of *S. aureus* (SEQ. ID. No. 88), *B. subtilis* (SEQ. ID. No. 89), and *E. coli* (SEQ. ID. No. 90). The conserved ATP site and the cystines forming the zinc finger are indicated above the sequence. The organisms used in the alignment were: *E. coli* (GenBank); and *B. subtilis*.

Please replace the paragraph at page 22, lines 1–3 with the following amended paragraph:

Figure 11 compares the homology between the DnaB polypeptide of *S. aureus* (SEQ. ID. No. 91) and other organisms. The organisms used in the alignment were: *E. coli* (GenBank) (SEQ. ID. No. 92); *B. subtilis* (SEQ. ID. No. 93); *Sal.Typ.*, (*Salmonella typhimurium*) (SEQ. ID. No. 94).

Please replace the paragraph at page 22, lines 4–9 with the following amended paragraph:

Figures 12A-B show the alignment of the delta subunit encoded by *holA* for *E. coli* (SEQ. ID. No. 95) and *B. subtilis* (SEQ. ID. No. 96) (Figure 12A) and for the delta subunit of *B. subtilis* (SEQ. ID. No. 96) and *S. pyogenes* (SEQ. ID. No. 97) (Figure 12B). Figure 12A shows ClustalW generated alignment of ~~*S. pyogenes*~~ *B. subtilis* (Gram positive) delta (SEQ. ID. No. 96) to *E.coli* (Gram negative) delta (SEQ. ID. No. 95). Figure 12B shows ClustalW generated alignment of *B. subtilis* (Gram positive) delta (SEQ. ID. No. 96) to *S. pyogenes* (Gram positive) delta (SEQ. ID. No. 97).

Please replace the abstract of the disclosure with the following amended abstract:

The present invention relates to ~~alpha-large, alpha-small, delta, delta prime, tau,~~ beta~~, SSB, DnaG, and DnaB~~ protein-encoding genes from Gram positive bacterium~~,~~ ~~preferably *Streptococcus* and *Staphylococcus* bacterium. The formation of functional polymerase as well as the use of such a polymerase in sequencing and amplification is also disclosed. The individual genes and proteins or polypeptides are useful in identification of compounds with antibiotic activity.~~ Expression systems and host cells containing these genes are also disclosed.